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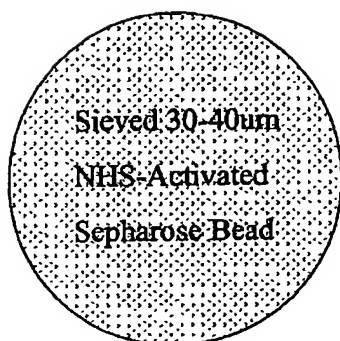
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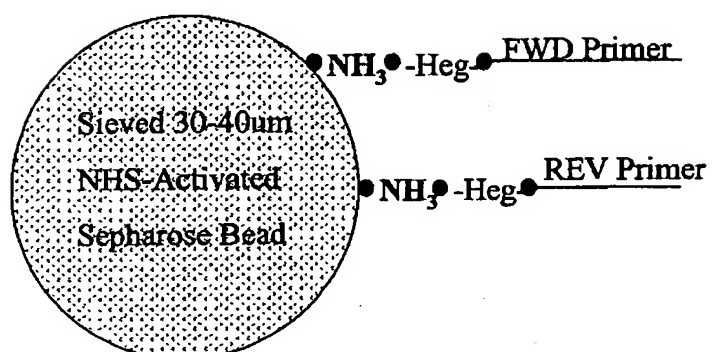
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FIGURE 1

A



B



C

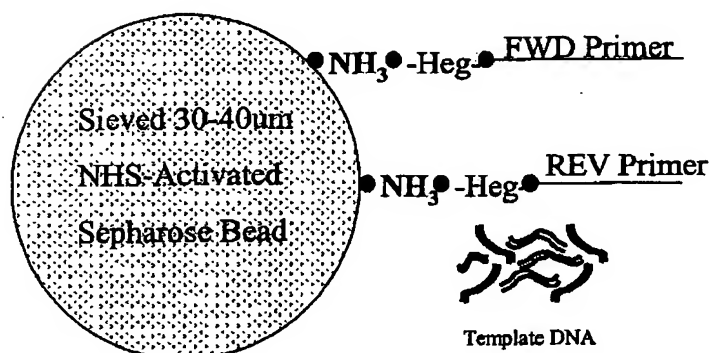
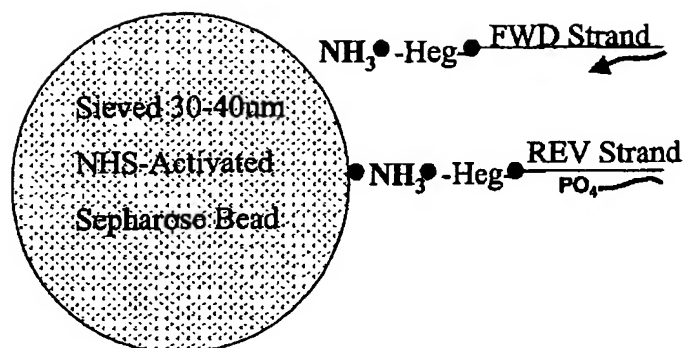
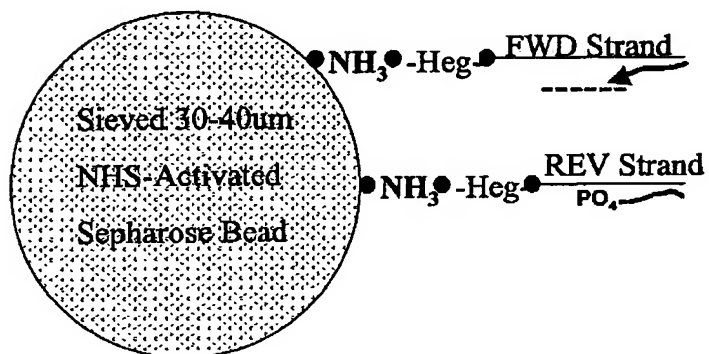


FIGURE 1

D



E



F

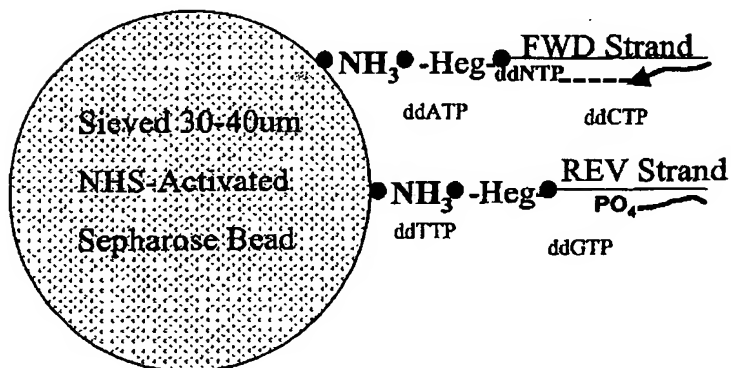
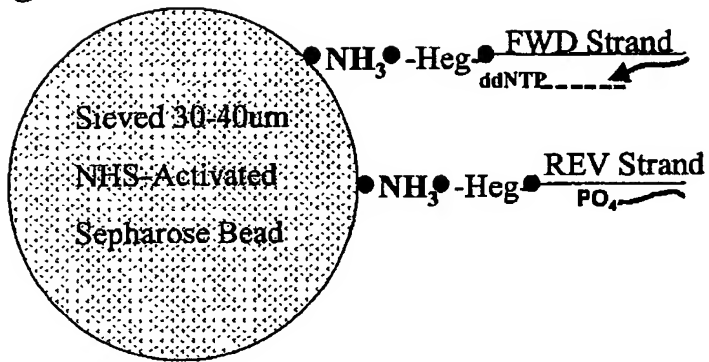
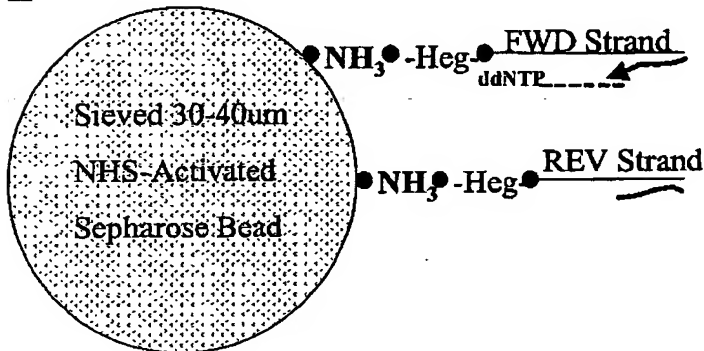


FIGURE 1

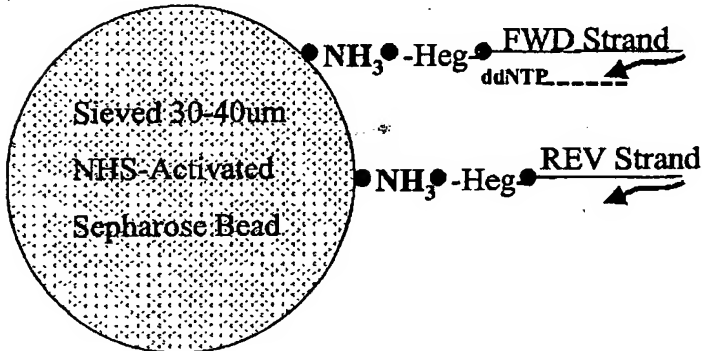
G



H



I



J

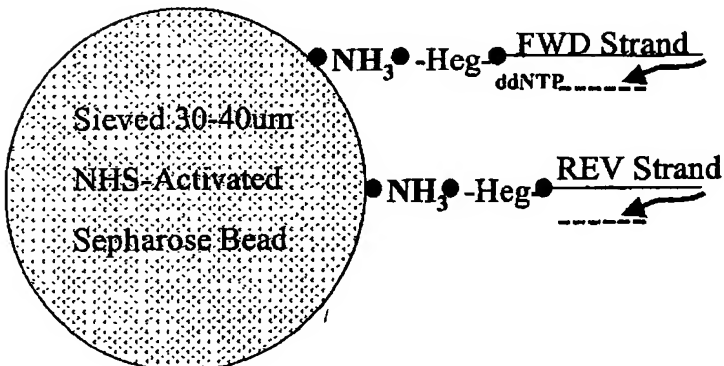


FIGURE 2

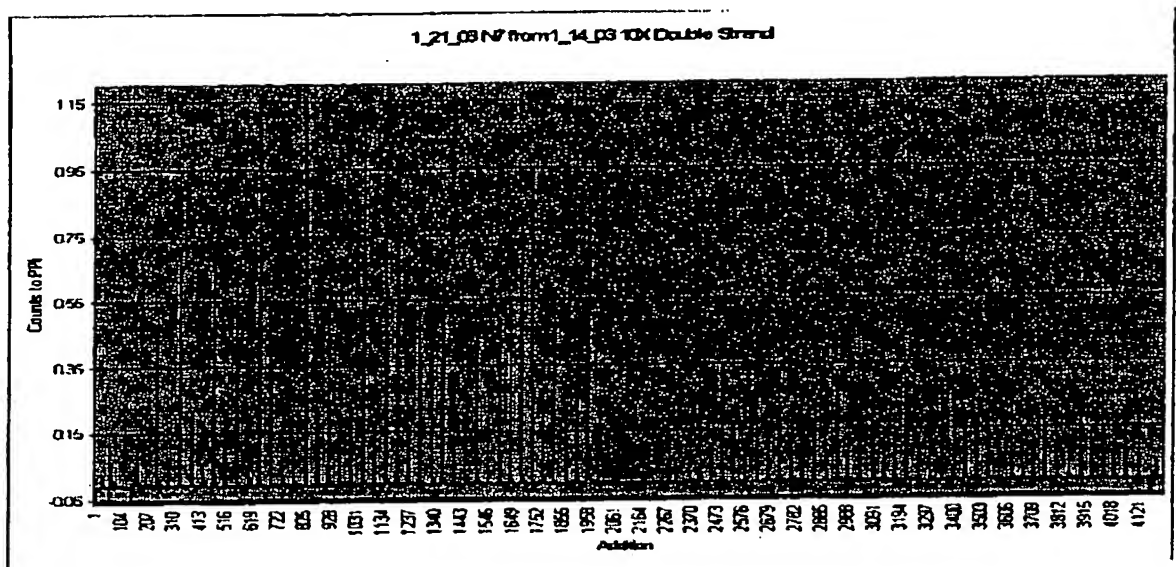
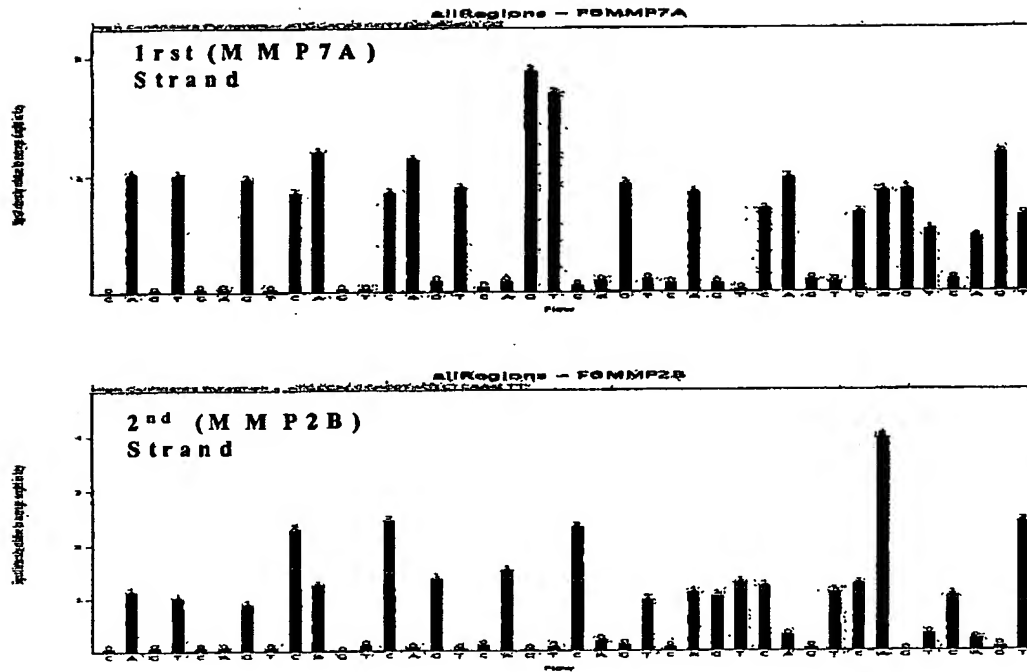


FIGURE 3

A)



1st Strand
(MMP7A)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00001_1362_1660.well	ATGCACATGGTTGACACAGTGGT	22

ATGC ACATGGTTGACACAGTGG

ATGC CACGACCTAGTCTCAA

2nd Strand
(MMP2B)

Sample	Well Location	Sequence	Perfect Match Length
F6_14_1	00003_1363_1660.well	ATGCCACCGACCTAGTCTCAA	25

FIGURE 4

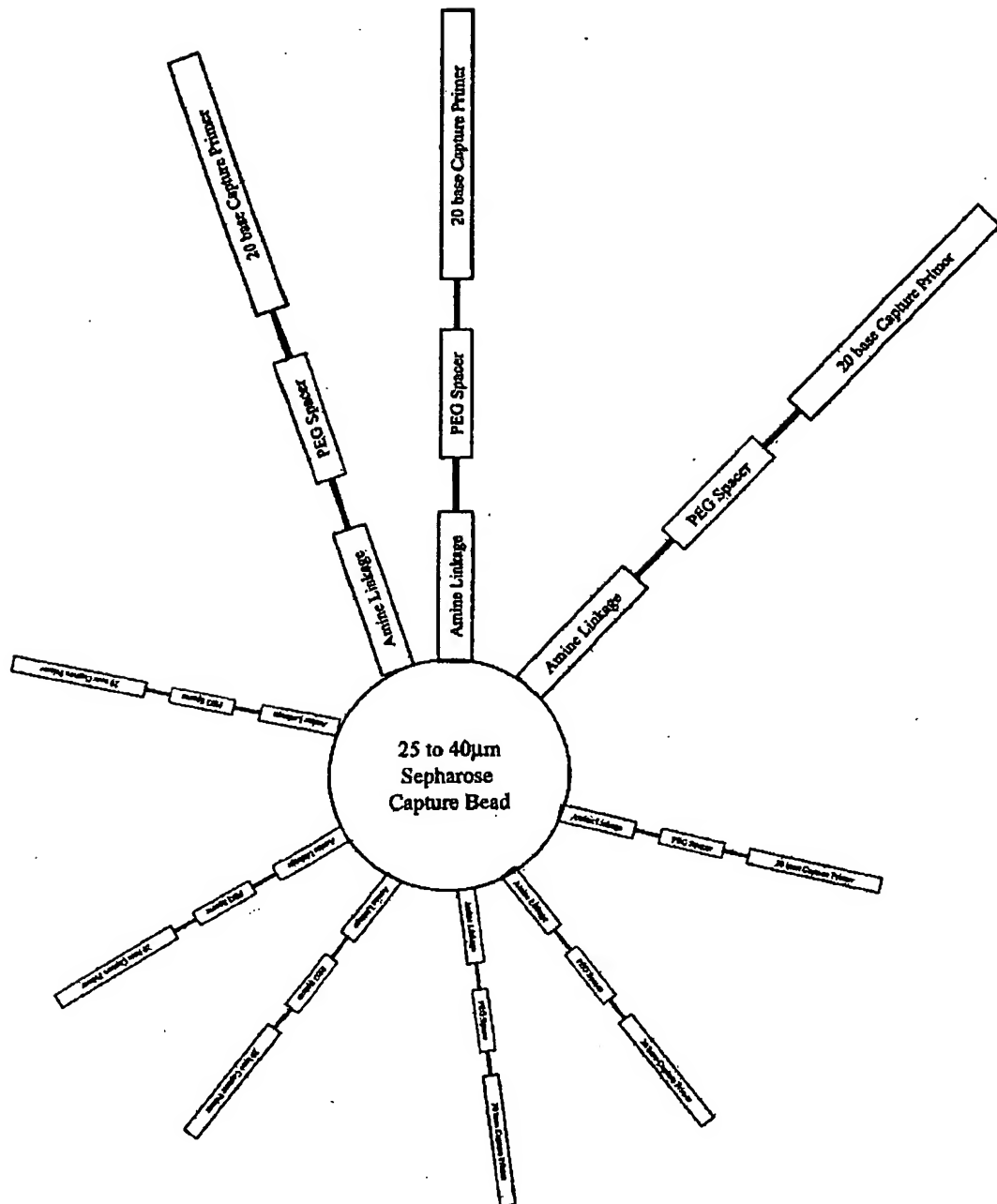


Fig. 5

A

B

C

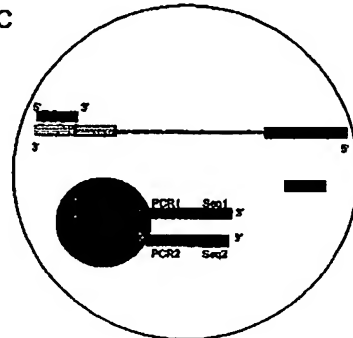
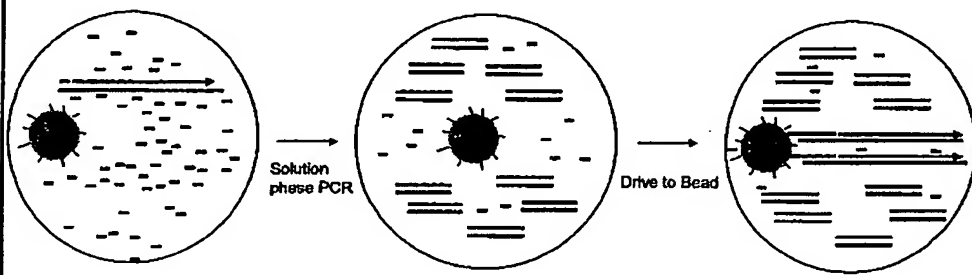


Fig. 6



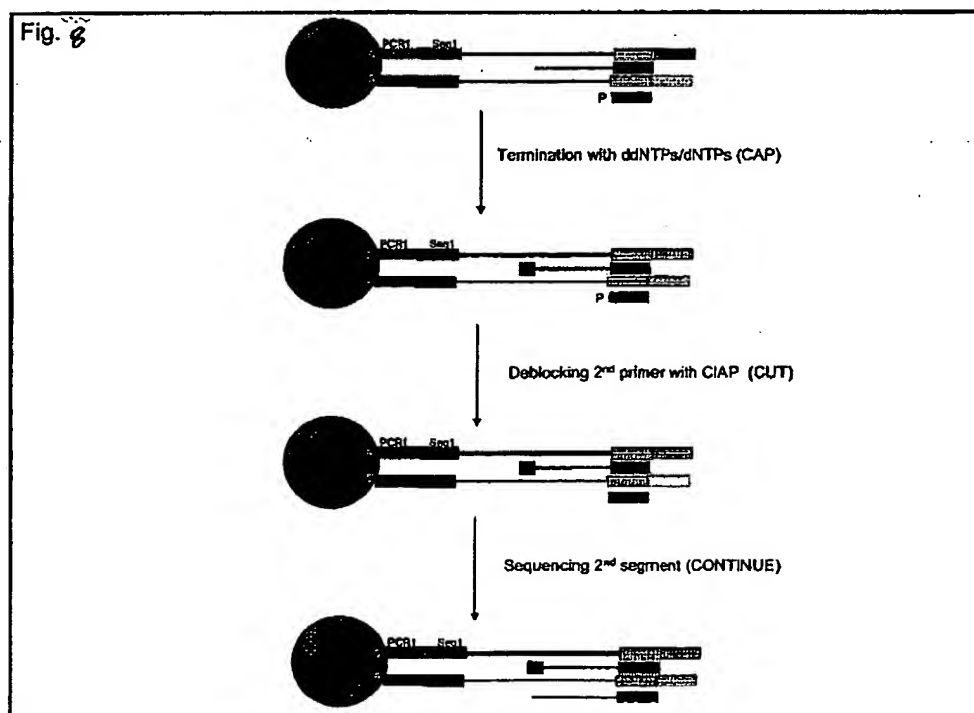
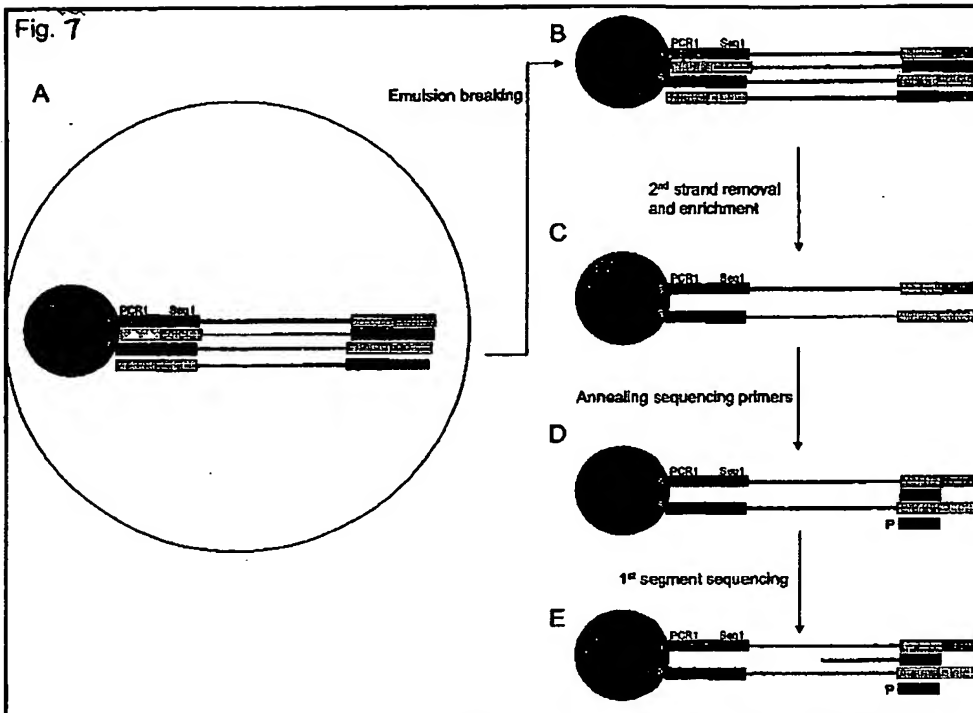
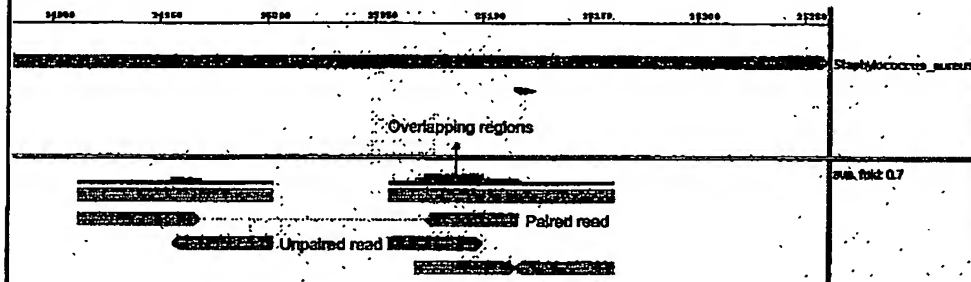


Fig. 9

A



B

Total Reads	31,785
Total 1st Strand	15,770
Total 2nd strand	16,015
Paired	11,799
Non Paired Reads	8,187
Total Coverage	38%

Fig. 10

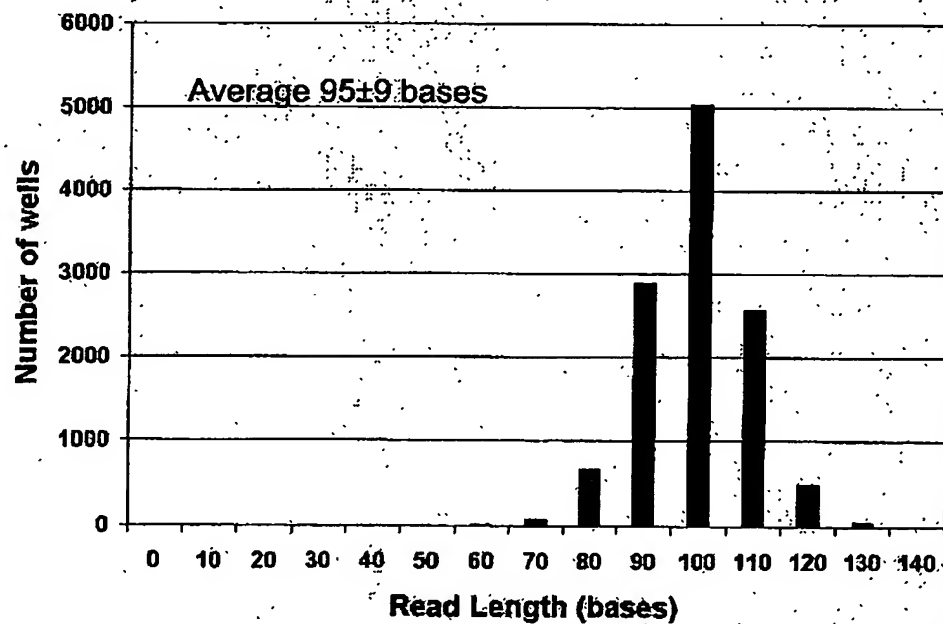


Fig. 11

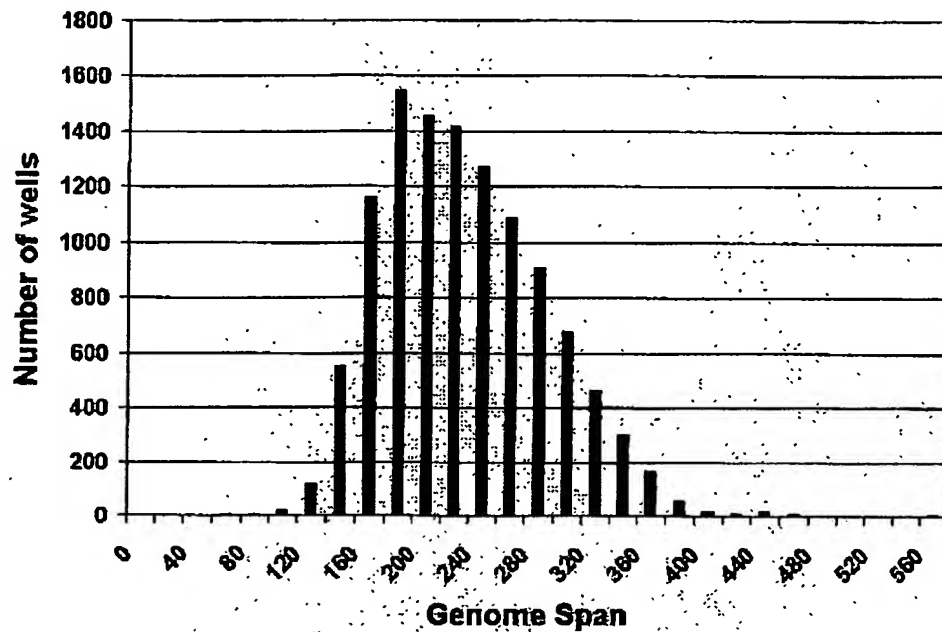


Fig. 12

Well	Genome Position	Orientation	Alignment String
00364 0548 2509	571366	F	TATTGTTGATGCTGTAAAAAAGAGCTACTGGTGTAGTATTTTATGAAGTT
00384 0548 2509 D2	571512	R	TGCTCAAAGAATTCATTTAAATATGACCATAATTCATTGTATCTTT
00389 0985 2232	1487890	R	AAGCGAACAGTCAAGTACCACAGTCAGTTGACITTAACACAAGCGGAT
00383 0985 2232 D2	1487769	F	TACAGGTGTTGGTATGCCATTTGCQATTGTTGCGGTTGGTTAGCCG
00397 0940 2923	2611033	F	AACATATAACATGCCCTATGTCAATTCGCTTCATGTAACAAAAAAGC
00397 0940 2923 D2	2611164	R	TAGATATCACTTGCCTGTTACTGTAATGCAGGCATGAG
00417 0611 1933	122001	R	ATTCAACTCTGGAATGCTTCTTGATACGCCTEGATGATG
00417 0611 1933 D2	121930	F	GATGAGGAGCTGCAATGSCAATGGGTAAAGGCATCATCG
00434 0695 0993	2022591	R	TGTATCTCGATTGCGATTAGTTGCTTTTGCATCTTCATTAGACC
00434 0695 0993 D2	2022473	F	CATTAAACATCTGCACCAGAAATAGCTTCTAATACGATTGC
00443 1003 0754	107373	F	GCBACGACGTCCAGCTAATAACBCTGCACCTAAGGCTAATGATAAT
00443 1003 0754 D2	107502	R	AAACCATGCAGATGCTAACAAAGCTCAAGCATTACCAGAAACT
00454 1257 3047	59038	R	TGTTGCTGCATCATAATTTAATACTACATCATTTAAATGTTTGG
00454 1257 3047 D2	58880	F	GCAGATGGTGTGACTAACCAAGTTGGTCAAAATGCCCTAAATACAAAAGAT